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## SEARCH REQUEST FORM

### Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner # : \_\_\_\_\_ Date: \_\_\_\_\_  
Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Mail-Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

<b>STAFF USE ONLY</b>		<b>Type of Search</b>	<b>Vendors and cost where applicable</b>
Searcher:	_____	NA Sequence (#)	STN _____
Searcher Phone #:	_____	AA Sequence (#)	Dialog _____
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Date Searcher Picked Up:	_____	Bibliographic	Dr.Link _____
Date Completed:	4/8	Litigation	Lexis/Nexis _____
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Clerical Prep Time:	_____	Patent Family	WWW/Internet _____
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GenCore version 5.1.4\_p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2003, 23:47:29 ; Search time 83 Seconds

(without alignments)  
 6384.788 Million cell updates/sec

Title: US-09-847-081B-1

Perfect score: 1728

Sequence: 1 agaaaccaaagaacac.....tcatcaaacctcaagttag 1728

Scoring table: IDENTITY\_NUC

Gapext 1.0

Searches: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*

2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*

3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*

4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*

5: /cgn2\_6/ptodata/1/ina/PCMS\_COMB.seq:\*

6: /cgn2\_6/ptodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	868	50.2	1826	1	US-09-579-667-5	Sequence 5, Appl1	Sequence 5, Appl1
2	858.6	49.7	1795	1	US-09-579-667-1	Sequence 1, Appl1	Sequence 1, Appl1
3	853.4	49.4	1834	1	US-09-579-667-7	Sequence 7, Appl1	Sequence 7, Appl1
4	842	48.7	1666	1	US-09-595-950-2	Sequence 2, Appl1	Sequence 2, Appl1
5	842	48.7	1646	1	US-09-300-542-2	Sequence 2, Appl1	Sequence 2, Appl1
6	811.2	46.9	1316	1	US-09-180-342-2	Sequence 2, Appl1	Sequence 2, Appl1
7	811.2	46.9	1316	1	US-09-579-667-3	Sequence 3, Appl1	Sequence 3, Appl1
8	415.2	24.0	1239	4	US-09-180-342-1	Sequence 1, Appl1	Sequence 1, Appl1
9	172	10.0	749	1	US-09-579-667-9	Sequence 9, Appl1	Sequence 9, Appl1
c 10	54	3.1	7218	1	US-09-232-463-14	Sequence 14, Appl1	Sequence 14, Appl1
c 11	52.4	3.0	114	2	US-09-260-546-10	Sequence 10, Appl1	Sequence 10, Appl1
12	52.4	3.0	114	4	US-09-436-068A-12	Sequence 12, Appl1	Sequence 12, Appl1
13	37.2	2.2	891	1	US-09-783-705A-11	Sequence 11, Appl1	Sequence 11, Appl1
14	37.2	2.2	1232	4	US-09-908-758-11	Sequence 1, Appl1	Sequence 1, Appl1
15	37.2	2.2	6918	1	US-09-783-705A-13	Sequence 13, Appl1	Sequence 13, Appl1
16	36	2.1	1955	3	US-09-166-460-11	Sequence 1, Appl1	Sequence 1, Appl1
17	36	2.1	1959	4	US-09-361-718-11	Sequence 1, Appl1	Sequence 1, Appl1
18	36	2.1	1959	4	US-09-398-395A-27	Sequence 27, Appl1	Sequence 27, Appl1
c 19	35.4	2.0	2468	1	US-09-468-036-19	Sequence 19, Appl1	Sequence 19, Appl1
c 20	35.4	2.0	2468	2	US-09-376-843-19	Sequence 19, Appl1	Sequence 19, Appl1
c 21	35.4	2.0	2469	1	US-09-447-500-3	Sequence 3, Appl1	Sequence 3, Appl1
c 22	35.4	2.0	2469	1	US-09-454-097-3	Sequence 3, Appl1	Sequence 3, Appl1
c 23	33.4	2.0	2469	1	US-09-453-866-3	Sequence 3, Appl1	Sequence 3, Appl1
c 24	35.4	2.0	2469	3	US-09-185-359-37	Sequence 37, Appl1	Sequence 37, Appl1
c 25	34.8	2.0	654	4	US-09-134-001C-2655	Sequence 2655, Appl1	Sequence 2655, Appl1
c 26	34	2.0	1056	4	US-09-961-527-48	Sequence 48, Appl1	Sequence 48, Appl1
c 27	33.4	1.9	25002	4	US-09-961-527-48	US-09-579-667-5	US-09-579-667-5

Query Match Best Local Similarity 50.2% ; Score 868; DB 1; Length 1826; Pred. No. 3.8e-239;

Best Local Similarity 77.2% ; Score 868; DB 1; Length 1826; Pred. No. 3.8e-239;

#### ALIGNMENTS

RESULT 1  
 US-09-579-667-5  
 Sequence 5, Application US/08579567  
 ; Patent No. 5105624

#### GENERAL INFORMATION:

APPLICANT: Fitzmaurice, Wayne P.  
 HELLMANN, Gary M.  
 Grill, Laurence K.  
 Kumagai, Monto H.  
 APPLICANT: Della-Cioppa, Guy R.  
 TITLE OF INVENTION: DNA SEQUENCES ENCODING ENZYMES USEFUL IN PHYTOENE BIOSYNTHESIS

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Virginia C. Bennett  
 STREET: 1211 East Morehead Street, PO Drawer 31009  
 CITY: Charlotte  
 STATE: No 5705624th Carolina  
 COUNTRY: USA  
 ZIP: 28234

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-POS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/579, 667  
 FILING DATE: 13/07/1998  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bennett, Virginia C.  
 REGISTRATION NUMBER: 37,092  
 REFILE/DOCKET NUMBER: 627-196  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 919-420-2200  
 TELEFAX: 919-881-3175  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1826 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 367..1596

Matches 1187; Conservative 0; Mismatches 255; Indels 96; Gaps 7;

QY 109 TGGAAATTAGTGGATAGACTCTACTGGATATCACAAAGTATTGGTTTGTAAATAG 168  
 Db 221 TAACTCTAGTGGAACTCTAGAGGATTTTATTTTTATTTTAAATTA 280

QY 169 GCTGAGGGAGAAGGTAACATAA-----GGAAGAACAAACTGGGAAATTGTTT 220  
 Db 281 GCAAGGAGGGAGAACAGAAGAACAGAAAGTAAAGACAAACCTGGAAATGTTT 340

QY 221 AGGACCCACGGGTTCTGTTATGAGCATGCTGTTGCTTGTGGGTTTC 280  
 Db 341 AGAACACCAAGGTTGTTGTC---AGATGCTGTTGCCTGTTATGGGTTTCAC 397

QY 281 CCACTCCGGGGCTGAATGGACAGGATGTTGATTCACTGCCAGAAAGGAAACCG 340  
 Db 398 ---CTTGAGGAGGCTCAATGGACAGGATCTTGTGTTCAAGGGAGGAACGG 454

QY 341 TCTTGTATCATCAGGTTCTAGCTCGAGATGAGGAATTGAGTGGATGAGA 400  
 455 TTGTTGACTCGTGAGG-----CATAGAATTAGTGTGTCATGAGAGATC 502

QY 401 AGAAAGGGGAGAACAAAGTGGGAAATTGGCTTTAATGTTGATCAAGATATC 460  
 503 AAGAGGTTGAAACAAAGGTGATTGG----- 533

QY 461 GCTTGGGGATCAGAAGACTGAAGGGAGCACTTCCTGAGCAGCTGGGG 520  
 Db 534 -----TTCTGAGGGCTGCGATGGGG 556

QY 521 CTACCCACCTGAGAAT---GACTGTCATCAGAAGAAAGGTGTTGAGTGGAT 577  
 Db 557 CTACACCAACGGAGAACATGGACATGACATGAGAACAGAAGGTTATGTTG 616

QY 578 TAAGCAGSCAGCTTAGGAAAGGGAGCTGGATCACCGATGATTAGAGTGAGC 637  
 Db 617 TGAACACAGCAGCTTAGGAAAGGAGACTGAGATCTACTGAGATTAGAGTGAGC 676

QY 638 CGGATATGTTGTCAGGAAATTGGCTGTTGAGGAGGATATGATCGTGTGGGG 697  
 Db 677 CGGAGATCCTCTCCCGGGAAATTGACTGTTAAGGATATCATGTTGAGT 736

QY 698 AAGTAACTGAGACTATGAAAGCATTTACTAGAACCAAGCTAATGACCCAGA 757  
 Db 737 AAGATGGCCAGAGTATGCAAAACATTTACTAGAACCTATGACTCCAGAGA 796

QY 758 GAAGAGAGCTATGGCAATATGTTGGCAGGAGAACGGATGCTGTGAGT 817  
 797 GAGAGAGCTATGGCAATATGTTGGCAGGAGAACGGATGACTGTGAGT 856

QY 818 GGCCTAATGCACTCCACATRACTCGCAAGCTTGTAGAATGGTGAGCACTGGAG 877  
 Db 857 GCGCAATGCACTACATRACTCGCAACGCTTGTAGAATGGTGAGCACTGGAG 916

QY 878 ATTTTCACTGGGGCATTTGATGAGCTTGTAGCTGCTTGTGGATGCTCA 937  
 917 ATGTTTCACTGGGGCATTTGATGAGCTTGTGGATGCTTGTGGATGCTTC 976

QY 938 GATTCCTCTGTGATAATGCCATTGAGATGAGGATGGTATGACTGT 997  
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QY 998 GGAATCCGATCAAAACTTGTAGCTATCTATGTTGCTGCTA 1057  
 Db 1037 GGAGTCACTACATRACTCGCAACGCTTGTAGACTATACCTATATTAC 1096

QY 1058 CTGTTAGGATTGAGTGTGCTTGTGGATGCTGAACTGATCAAGGACACAG 1117  
 Db 1097 CGGTGGGGTGTGAGTGTCCATTATGGGTTATGCACTGATCAAGGACACAG 1156

QY 1118 AGGTGTATATAATGCTGCTTGTGGATGCTGAACTGATCAACCAATACTCA 1177  
 Db 1157 AGGTGTATATAATGCTGCTTGTGGATGCTGAACTGATCAACCAATACTCA 1216

## RESULT 2

US-08-579-667-1

Sequence 1, Application US/08579667  
 Patent No. 5705624

## GENERAL INFORMATION:

APPLICANT: Fitzmaurice, Wayne P.

APPLICANT: Hellmann, Gary M.

APPLICANT: Grill, Laurence K.

APPLICANT: Kumagai, Monto H.

APPLICANT: Della-Cioppa, Guy R.

TITLE OF INVENTION: DNA SEQUENCES ENCODING ENZYMES USEFUL IN

NUMBER OF INVENTION: PHYTOENE BIOSYNTHESIS

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Virginia C. Bennett

STREET: 1211 East Morehead Street, PO Drawer 34009

CITY: Charlotte

STATE: No. 5705624th Carolina

COUNTRY: USA

ZIP: 28224

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.3.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/579,667

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Bennett, Virginia C.

REGISTRATION NUMBER: 37,092

REFERENCE/DOCKET NUMBER: 627-196

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-881-2200

TELEFAX: 919-881-3175

INFORMATION FOR SEO ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1795 base pairs